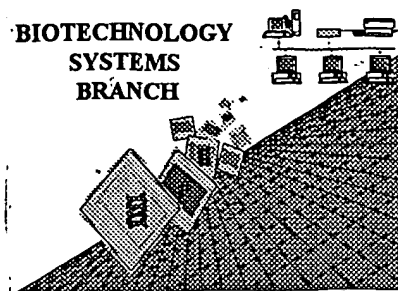


RAW SEQUENCE LISTING **ERROR REPORT**



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/009,330
Source: PCR/10
Date Processed by STIC: 1/14/2002

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 3.1 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom, including:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:
U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
Or
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

ERROR DETECTED**SUGGESTED CORRECTION**

SERIAL NUMBER:

10/009330

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos
The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length
The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
 Numbering
The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII
The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length
Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
 "bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences
 (OLD RULES)
Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading).
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences
 (NEW RULES)
Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 9 Use of n's or Xaa's
 (NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 Invalid <213>
 Response
Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220>
Sequence(s) 10 missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
 "bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n
n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

PCT10

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/009,330

DATE: 01/14/2002

TIME: 13:43:57

Input Set : A:\Sequence Listing.txt

Output Set: N:\CRF3\01142002\J009330.raw

Does Not Comply
Corrected Diskette Needed

3 <110> APPLICANT: Takeda Chemical Industries, Ltd.
W--> 4 <120> TITLE OF INVENTION: Screening Method Using CD100
W--> 5 <130> FILE REFERENCE: 2611WOOP
C--> 6 <140> CURRENT APPLICATION NUMBER: US/10/009,330
C--> 6 <141> CURRENT FILING DATE: 2001-12-03
6 <150> PRIOR APPLICATION NUMBER: JP 11-157111
7 <151> PRIOR FILING DATE: 1999-06-03
W--> 8 <160> NUMBER OF SEQ.ID: 10

ERRORED SEQUENCES

413 <210> SEQ ID NO: 6 1337 shown
414 <211> LENGTH: 1357
415 <212> TYPE: DNA
416 <213> ORGANISM: Mouse
W--> 417 <400> SEQUENCE: 6
418 tggagactg tgaagcagag ggcgccaggg ctatggctga cgctatcacg tatgcagacc 60
419 tgcgctttgt gaaagtgtcc ctgaagaaca ggcgatctaa ccatctagga caggactgtg 120
420 aggcctatga agatggggaa ctcacctacg agaatgtgca agtgtctcca gtcccaggag 180
421 ggccaccagg cttggcttcc cctgcactag cggacaaagc aggggtcggg tcagagcaac 240
422 caactgcgac ctggagctct gtgaactcgt ctgctctcag gcagattccc cgctgtccta 300
423 cagtctgctt gcaatacttc ttgcttggcc ttctcgtgtc ctgtctgatg ttaggggtgg 360
424 ctgtcatctg cctgggagtt cgctatctgc aggtgtctcg gcagttccag gaggggacca 420
425 ggatttggga agccaccaat agcagcctgc agcagcagct caggggagaag ataagtcagc 480
426 tggggcagaa ggaggtggag cttcagaagg ctcggaagaa gctgatctcg agccaggaca 540
427 cattacagga gaagcagagg actcacgagg acgctgagca gcaactacaa gcctgccagg 600
428 ctgagagagc gaagaccaag gagaacctga aaactgagga ggagcggagg agggacctgg 660
429 accagaggtt gacaagcacg cgggagacac tgaggcgctt cttctctgat tcatcagaca 720
430 cctgctgtcc atgcggatgg attccatata aggaaaggtg cttttacata tcacataccc 780
431 tcggaagtct ggaggagagc caaaaatact gcacatctct gtccctccaa ctggcagcat 840
432 tcgatgaacc ttctaagtat tactatgaag tttctctgcc cagcggctta gaggagtgtc 900
433 tagatcgttc gaagtcatat tggatacaga tgagcaagaa gtggaggcag gactctgact 960
434 ctcaaagccg acattgtgtc aggataaaaa catattacca gaagtgggaa agaacaattt 1020
435 ccaagtgtgc agagcttcac ccctgcattt gtgagtcgga ggctttcagg tttcctgatg 1080
436 ggatcaatct gaactgaaac ggacacttga acaagacctt gtgacctaca tccttaacct 1140
437 acggcctgcc aatttttaag actgctatcc ctccagcact ccctcactct cgggcatgcc 1200
438 cagctaaggg atgacctgct gcttgcttga aagctgctcc agaaactgga cttctcttgg 1260
E--> 439 gaagagtaaa gaagcctcca gaaaagactt gaccttcctt aagaacttcc caaactagag 1340 1320
E--> 440 atgggtcagg ggagggc 1357 1337
531 <210> SEQ ID NO: 10
532 <211> LENGTH: 53
533 <212> TYPE: DNA
534 <213> ORGANISM: Artificial Sequence
W--> 535 <220> FEATURE:
536 <223> OTHER INFORMATION:
W--> 537 <400> SEQUENCE: 10

see item 11 on Error Summary Sheet
see next page

RAW SEQUENCE LISTING

DATE: 01/14/2002

PATENT APPLICATION: US/10/009,330

TIME: 13:43:57

Input Set : A:\Sequence Listing.txt

Output Set: N:\CRF3\01142002\J009330.raw

538 gacggatcct acttactttg ctttgcttgc ttgagataca ccgtcttctc tga 53
E--> 543 ①

delete

VERIFICATION SUMMARY

DATE: 01/14/2002

PATENT APPLICATION: US/10/009,330

TIME: 13:43:58

Input Set : A:\Sequence Listing.txt

Output Set: N:\CRF3\01142002\J009330.raw

L:4 M:283 W: Missing Blank Line separator, <120> field identifier
L:5 M:283 W: Missing Blank Line separator, <130> field identifier
L:6 M:270 C: Current Application Number differs, Replaced Current Application No
L:6 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:8 M:283 W: Missing Blank Line separator, <160> field identifier
L:9 M:283 W: Missing Blank Line separator, <210> field identifier
L:13 M:283 W: Missing Blank Line separator, <400> field identifier
L:126 M:283 W: Missing Blank Line separator, <400> field identifier
L:178 M:283 W: Missing Blank Line separator, <400> field identifier
L:291 M:283 W: Missing Blank Line separator, <400> field identifier
L:366 M:283 W: Missing Blank Line separator, <400> field identifier
L:417 M:283 W: Missing Blank Line separator, <400> field identifier
L:439 M:254 E: No. of Bases conflict, LENGTH:Input:1340 Counted:1320 SEQ:6
M:254 Repeated in SeqNo=6
L:440 M:252 E: No. of Seq. differs, <211>LENGTH:Input:1357 Found:1337 SEQ:6
L:445 M:283 W: Missing Blank Line separator, <400> field identifier
L:496 M:283 W: Missing Blank Line separator, <400> field identifier
L:527 M:283 W: Missing Blank Line separator, <220> field identifier
L:529 M:283 W: Missing Blank Line separator, <400> field identifier
L:535 M:283 W: Missing Blank Line separator, <220> field identifier
L:537 M:283 W: Missing Blank Line separator, <400> field identifier
L:543 M:254 E: No. of Bases conflict, LENGTH:Input:1 Counted:53 SEQ:10